L2    ANSWER 2 OF 20    CAPLUS    COPYRIGHT 2003 ACS         DUPLICATE 1
ACCESSION NUMBER:         2002:700274   CAPLUS
TITLE:                    The stress-response sigma factor .sigma.h controls the
                          expression of ssgB, a homologue of the
                          sporulation-specific cell division gene **ssgA**
                          , in streptomyces coelicolor A3(2)
AUTHOR(S):                Kormanec, J.; Sevcikova, B.
CORPORATE SOURCE:         Institute of Molecular Biology, Slovak Academy of
                          Sciences, Bratislava, 842 51, Slovakia
SOURCE:                   Molecular Genetics and Genomics (2002), 267(4),
                          536-543
                          CODEN: MGGOAA; ISSN: 1617-4615
PUBLISHER:                Springer-Verlag
DOCUMENT TYPE:            Journal; Miscellaneous
LANGUAGE:                 English

AB    By using a previously established method for the identification of
      promoters recognized by a particular sigma factor of RNA polymerase, we
      identified a promoter in Streptomyces coelicolor A3(2) that is recognized
      by a heterologous RNA polymerase contg. the late sporulation-specific
      sigma factor .sigma.F.  The promoter directed the expression of a gene
      named ssgB, which is related to the sporulation-specific cell division
      gene **ssgA**.  These genes, together with three others, constitute
      a new family of paralogous genes specific for Streptomyces.  S1-nuclease
      mapping using RNA prepd. from an Escherichia coli strain that expresses
      ssgB under the control of .sigma.F, and from S. coelicolor A3(2) at
      various developmental stages, identified identical transcription start
      points in both strains, corresponding to the promoter ssgBp.  The promoter
      is developmentally regulated in S. coelicolor: it is induced at the time
      of aerial mycelium formation and is most active during sporulation.
      However, the level of the ssgB transcript was unaffected in a sigF mutant
      of S. coelicolor A3(2).  Interestingly, the level of the transcript was
      substantially reduced in an S. coelicolor strain that was mutant for the
      sigH gene, which encodes a stress-response sigma factor (.sigma.H) that is
      essential for sporulation in S. coelicolor A3(2).  This dependence of ssgB
      upon sigH was confirmed by an in vitro transcription assay, in which
      .sigma.H, in the presence of the S. coelicolor core RNA polymerase, was
      able to recognize ssgBp.  These results suggest that the S. coelicolor
      ssgB gene is under the control of the stress-response .sigma.H.
      Transcription of ssgB was investigated in S. coelicolor A3(2) mutants with
      lesions in each of six known early whi genes required for sporulation
      septation.  Expression of ssgB was deregulated in three of the mutants
      (whiA, whiI, and whiJ).  Based on these data, it is proposed that the ssgB
      gene product plays a role in the developmental process in S. coelicolor
      A3(2).
REFERENCE COUNT:          27    THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS
                                RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT


L2    ANSWER 1 OF 20    SCISEARCH   COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER:         2002:944103   SCISEARCH
THE GENUINE ARTICLE:      614ZL
TITLE:                    Protein analysis in a pleomorphically deteriorated strain
                          of the insect-pathogenic fungus Metarhizium anisopliae
AUTHOR:                   Kamp A M; Bidochka M J (Reprint)
CORPORATE SOURCE:         Brock Univ, Dept Biol Sci, St Catharines, ON L2S 3A1,
                          Canada (Reprint)
COUNTRY OF AUTHOR:        Canada
SOURCE:                   CANADIAN JOURNAL OF MICROBIOLOGY, (SEP 2002) Vol. 48, No.
                          9, pp. 787-792.
                          Publisher: NATL RESEARCH COUNCIL CANADA, RESEARCH
                          JOURNALS, MONTREAL RD, OTTAWA, ONTARIO K1A 0R6, CANADA.
                          ISSN: 0008-4166.
DOCUMENT TYPE:            Article; Journal

LANGUAGE:          English
REFERENCE COUNT:   14
                        *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB      Pleomorphic deterioration is a process where a fungal isolate loses the
        ability to produce conidia during repeated subculturing. We have
        previously isolated strains of the entomopathogenic fungus Metarhizium
        anisopliae that have irreversibly lost the ability to produce conidia and
        only produce mycelia when grown on agar. Gel electrophoresis was used to
        examine differences in intracellular protein patterns (urea-soluble
        proteins and urea-insoluble proteins (i.e. hydrophobins)) in conidating
        and mycelial cultures of M. anisopliae. Two major proteins present in a
        conidiating culture and one from a mycelial culture were N-terminally
        sequenced but showed no homologies to known proteins. The presence of
        hydrophobins in conidating and mycelial cultures was also examined, and it
        was shown that these proteins were abundant in conidiating cultures but
        not in mycelial cultures. We also used primers designed from regulatory
        genes involved in conidiation in Aspergillus nidulans. The amplified
        fragments were not homologous to A. nidulans genes.

L2      ANSWER 2 OF 20   CAPLUS   COPYRIGHT 2003 ACS          DUPLICATE 1
ACCESSION NUMBER:          2002:700274   CAPLUS
TITLE:                     The stress-response sigma factor .sigma.h controls the
                           expression of ssgB, a homologue of the
                           sporulation-specific cell division gene **ssgA**
                           , in streptomyces coelicolor A3(2)
AUTHOR(S):                 Kormanec, J.; Sevcikova, B.
CORPORATE SOURCE:          Institute of Molecular Biology, Slovak Academy of
                           Sciences, Bratislava, 842 51, Slovakia
SOURCE:                    Molecular Genetics and Genomics (2002), 267(4),
                           536-543
                           CODEN: MGGOAA; ISSN: 1617-4615
PUBLISHER:                 Springer-Verlag
DOCUMENT TYPE:             Journal; Miscellaneous
LANGUAGE:                  English

AB      By using a previously established method for the identification of
        promoters recognized by a particular sigma factor of RNA polymerase, we
        identified a promoter in Streptomyces coelicolor A3(2) that is recognized
        by a heterologous RNA polymerase contg. the late sporulation-specific
        sigma factor .sigma.F.  The promoter directed the expression of a gene
        named ssgB, which is related to the sporulation-specific cell division
        gene **ssgA**.  These genes, together with three others, constitute
        a new family of paralogous genes specific for Streptomyces.  S1-nuclease
        mapping using RNA prepd. from an Escherichia coli strain that expresses
        ssgB under the control of .sigma.F, and from S. coelicolor A3(2) at
        various developmental stages, identified identical transcription start
        points in both strains, corresponding to the promoter ssgBp.  The promoter
        is developmentally regulated in S. coelicolor: it is induced at the time
        of aerial mycelium formation and is most active during sporulation.
        However, the level of the ssgB transcript was unaffected in a sigF mutant
        of S. coelicolor A3(2).  Interestingly, the level of the transcript was
        substantially reduced in an S. coelicolor strain that was mutant for the
        sigH gene, which encodes a stress-response sigma factor (.sigma.H) that is
        essential for sporulation in S. coelicolor A3(2).  This dependence of ssgB
        upon sigH was confirmed by an in vitro transcription assay, in which
        .sigma.H, in the presence of the S. coelicolor core RNA polymerase, was
        able to recognize ssgBp.  These results suggest that the S. coelicolor
        ssgB gene is under the control of the stress-response .sigma.H.
        Transcription of ssgB was investigated in S. coelicolor A3(2) mutants with
        lesions in each of six known early whi genes required for sporulation
        septation.  Expression of ssgB was deregulated in three of the mutants
        (whiA, whiI, and whiJ).  Based on these data, it is proposed that the ssgB
        gene product plays a role in the developmental process in S. coelicolor
        A3(2).
REFERENCE COUNT:           27     THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS

ACCESSION NUMBER:       2001:820695  SCISEARCH
THE GENUINE ARTICLE:   481CL
TITLE:                 Simultaneous and multi-criteria optimization of TS
                       requirements and maintenance at NPPs
AUTHOR:                Martorell S (Reprint); Sanchez A; Carlos S; Serradell V
CORPORATE SOURCE:      Univ Politecn Valencia, Dept Chem & Nucl Engn, POB 22012,
                       Valencia 46071, Spain (Reprint); Univ Politecn Valencia,
                       Dept Chem & Nucl Engn, Valencia 46071, Spain; Univ
                       Politecn Valencia, Dept Stat & Operat Res, Valencia 46071,
                       Spain
COUNTRY OF AUTHOR:     Spain
SOURCE:                ANNALS OF NUCLEAR ENERGY, (JAN 2002) Vol. 29, No. 2, pp.
                       147-168.
                       Publisher: PERGAMON-ELSEVIER SCIENCE LTD, THE BOULEVARD,
                       LANGFORD LANE, KIDLINGTON, OXFORD OX5 1GB, ENGLAND.
                       ISSN: 0306-4549.
DOCUMENT TYPE:         Article; Journal
LANGUAGE:              English
REFERENCE COUNT:       48
                       *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB      One of the main concerns of the nuclear industry is to improve the
availability of safety-related systems at nuclear power plants (NPPs) to
achieve high safety levels. The development of efficient testing and
maintenance has been traditionally one of the different ways to guarantee
high levels of systems availability, which are implemented at NPP through
technical specification and maintenance requirements (TS&M). On the other
hand, there is a widely recognized interest in using the probabilistic
risk analysis (PRA) for risk-informed applications aimed to emphasize both
effective risk control and effective resource expenditures at NPPs.
TS&M-related parameters in a plant are associated with controlling risk or
with satisfying requirements, and are candidate to be evaluated for their
resource effectiveness in risk-informed applications. The resource versus
risk-control effectiveness principles formally enter in optimization
problems where the cost or the burden for the plant staff is to be
minimized while the risk or the availability of the safety equipment is
constrained to be at a given level, and vice versa. Optimization of TS&M
has been found interesting from the very beginning. However, the
resolution of such a kind of optimization problem has been limited to
focus on only individual TS&M-related parameters (STI, ACT, PM frequency,
etc.) and/or adopting an individual optimization criterion (availability,
costs, plant risks, etc.). Nevertheless, a number of reasons exist (e.g.
interaction, similar scope, etc.) that justify the growing interest in the
last years to focus on the simultaneous and multi-criteria optimization of
TS&M. In the simultaneous optimization of TS&M-related parameters based on
risk (or unavailability) and cost, like in many other engineering
optimization problems, one normally faces multi-modal and non-linear
objective functions and a variety of both linear and non-linear
constraints. Genetic algorithms (GAs) have proved their capability to
solve these kinds of problems, although GAs are essentially unconstrained
optimization techniques that require adaptation for the intended
constrained optimization, where TS&M-related parameters act as the
decision variables. This paper encompasses, in Section 2, the problem
formulation where the objective function is derived and constraints that
apply in the simultaneous and multi-criteria optimization of TS&M
activities based on risk and cost functions at system level. Fundamentals
of a steady-state GA (SSGA) as an optimization method is given
in Section 3, which satisfies the above requirements, paying special
attention to its use in constrained optimization problems. A simple case
of application is provided in Section 4, focussing on TS&M-related
parameters optimization for a stand-by safety-related system, which
demonstrates how the SSGA-based optimization approach works at

the system level, providing practical and complete alternatives beyond only mathematical solutions to a particular parameter. Finally, Section 5 presents our conclusions.

ACCESSION NUMBER:       2002:947738   SCISEARCH
THE GENUINE ARTICLE:    616BT
TITLE:                  Deprogrammed sporulation in Streptomyces
AUTHOR:                 Ohnishi Y; Seo J W; Horinouchi S (Reprint)
CORPORATE SOURCE:       Univ Tokyo, Grad Sch Agr & Life Sci, Dept Biotechnol, Bunkyo Ku, Tokyo 1138657, Japan (Reprint)
COUNTRY OF AUTHOR:      Japan
SOURCE:                 FEMS MICROBIOLOGY LETTERS, (29 OCT 2002) Vol. 216, No. 1, pp. 1-7.
                        Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS.
                        ISSN: 0378-1097.
DOCUMENT TYPE:          General Review; Journal
LANGUAGE:               English
REFERENCE COUNT:        23
                        *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB      The bacterial genus Streptomyces forms chains of spores by septation at intervals in aerial hyphae and subsequent maturation on solid medium. Substrate hyphae undergo extensive lysis, liberating nutrients on which aerial hyphae develop. Some mutant strains, however, ectopically form spores by septation in substrate hyphae on solid medium or in vegetative hyphae in liquid medium, which suggests that all hyphae have the potential to differentiate into spores. A Streptomyces griseus mutant strain NP4, which has a mutation in the regulatory system for an ATP-binding cassette (ABC) transporter gene, forms ectopic spores in substrate hyphae only on glucose-containing medium. In addition, overexpression of a substrate-binding protein of the ABC transporter in the wild-type strain causes ectopic septation in very young substrate hyphae and subsequent sporulation in response to glucose. These ectopic spores germinate normally. The ectopic sporulation is independent of A-factor, a microbial hormone that determines the timing of aerial mycelium formation during normal development. Thus, substrate hyphae of Streptomyces have a potential to develop into spores without formation of aerial hyphae. For programmed development, therefore, the strict repression of septum formation in substrate mycelium should be necessary, as well as the positive signal relay leading to aerial mycelium formation followed by septation and sporulation. (C) 2002 Federation of European Microbiological Societies. Published by Elsevier Science B.V. All rights reserved.

ACCESSION NUMBER:       2001:806965   SCISEARCH
THE GENUINE ARTICLE:    478BA
TITLE:                  Improvements in genetic algorithms
AUTHOR:                 Vasconcelos J A (Reprint); Ramirez J A; Takahashi R H C; Saldanha R R
CORPORATE SOURCE:       Univ Fed Minas Gerais, Dept Engn Eletr, Av Antonio Carlos 6627, BR-31270901 Belo Horizonte, MG, Brazil (Reprint); Univ Fed Minas Gerais, Dept Engn Eletr, BR-31270901 Belo Horizonte, MG, Brazil
COUNTRY OF AUTHOR:      Brazil
SOURCE:                 IEEE TRANSACTIONS ON MAGNETICS, (SEP 2001) Vol. 37, No. 5, Part 1, pp. 3414-3417.
                        Publisher: IEEE-INST ELECTRICAL ELECTRONICS ENGINEERS INC, 345 E 47TH ST, NEW YORK, NY 10017-2394 USA.
                        ISSN: 0018-9464.
DOCUMENT TYPE:          Article; Journal
LANGUAGE:               English
REFERENCE COUNT:        6

AB    This paper presents an exhaustive study of the Simple Genetic Algorithm (SGA), Steady State Genetic Algorithm (**SSGA**) and Replacement Genetic Algorithm (RGA). The performance of each method is analyzed in relation to several operators types of crossover, selection and mutation, as well as in relation to the probabilities of crossover and mutation with and without dynamic change of its values during the optimization process. In addition, the space reduction of the design variables and global elitism are analyzed. All GAS are effective when used with its best operations and values of parameters. For each GA, both sets of best operation types and parameters are found. The dynamic change of crossover and mutation probabilities, the space reduction and the global elitism during the evolution process show that great improvement can be achieved for all GA types. These GAs are applied to TEAM benchmark problem 22.

L2    ANSWER 6 OF 20   CAPLUS   COPYRIGHT 2003 ACS        DUPLICATE 2
ACCESSION NUMBER:        2001:407560  CAPLUS
DOCUMENT NUMBER:         135:133005
TITLE:                   Analysis of a genomic clone of hydrophobin (
                         **ssgA**) from the entomopathogenic fungus
                         Metarhizium anisopliae
AUTHOR(S):               Bidochka, Michael J.; De Koning, Jason; St. Leger,
                         Raymond J.
CORPORATE SOURCE:        Department of Biology, Trent University, Peterborough,
                         ON, K9J 7B8, Can.
SOURCE:                  Mycological Research (2001), 105(3), 360-364
                         CODEN: MYCRER; ISSN: 0953-7562
PUBLISHER:               Cambridge University Press
DOCUMENT TYPE:           Journal
LANGUAGE:                English
AB    A 909 bp region contg. a genomic clone encoding for hydrophobin (
      **ssgA**) from the entomopathogenic fungus Metarhizium anisopliae has
      been sequenced and the regulatory motifs analyzed against those recognized
      in other fungi.  The genomic clone was also compared with the open reading
      frame of the hydrophobin **ssgA** (starvation stress gene) cDNA
      sequence.  The genomic clone contained a 291 bp coding sequence with one
      intron of 64 nucleotides.  From this sequence primers were established
      that could be used to amplify the hydrophobin.  Restriction fragment
      polymorphism anal. of hydrophobin amplified by the polymerase chain
      reaction from 80 isolates of M. anisopliae showed no variability.  Anal.
      of the potential regulatory elements 313 bp upstream from the
      transcriptional start site revealed typical TATAA and CCAAT boxes.  CT or
      GC motifs were not found.  Upstream regulatory elements were also found
      with sequence homologies to the AREA, CREA, CRE (cAMP response element)
      and BRLA regions of Aspergillus nidulans as well as the CYS3 and AmyB
      regions of Aspergillus oryzae.  The promoter regions of other fungal
      hydrophobins were also assessed for the presence of regulatory elements.
      Upstream regulatory elements are also present for the gene encoding a
      cuticle-degrading protease (Pr1) from M. anisopliae.  We suggest that
      nutrient levels and cAMP mediation of thigmotropic signals in the
      entomopathogenic fungus, M. anisopliae, coordinate the regulation of the
      gene products required for morphol. development and secretion of
      "penetration" enzymes.
REFERENCE COUNT:         25    THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS
                         RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2    ANSWER 7 OF 20   CAPLUS   COPYRIGHT 2003 ACS        DUPLICATE 3
ACCESSION NUMBER:        2001:465413  CAPLUS
TITLE:                   Multi-objective evolutionary algorithms for MILP and
                         MINLP in process synthesis
AUTHOR(S):               Shi, Lei; Yao, Pingjing
CORPORATE SOURCE:        `Laboratory of Process System Engineering, Dalian
                         University of Technology, Dalian, 116012, Peop. Rep.
                         China

AB   Steady-state non-dominated sorting genetic algorithm (SNSGA), a new form
     of multi-objective genetic algorithm, is implemented by combining the
     steady-state idea in steady-state genetic algorithms (**SSGA**) and
     the fitness assignment strategy of non-dominated sorting genetic algorithm
     (NSGA).  The fitness assignment strategy is improved and a new
     self-adjustment scheme of .sigma.shone is proposed.  This algorithm is
     proved to be very efficient both computationally and in terms of the
     quality of the Pareto fronts produced with five test problems including GA
     difficult problem and GA deceptive one.  Finally, SNSGA is introduced to
     solve multi-objective mixed integer linear programming (MILP) and mixed
     integer non-linear programming (MINLP) problems in process synthesis.
REFERENCE COUNT:         21    THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS
                               RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB   One of the main concerns of the nuclear industry is to improve the
     availability of safety-related systems at nuclear power plants (NPPs) to
     achieve high safety levels.  The development of efficient testing and
     maintenance has been traditionally one of the different ways to guarantee
     high levels of systems availability, which are implemented at NPP through
     tech. specification and maintenance requirements (TS&M).  On the other
     hand, there is a widely recognized interest in using the probabilistic
     risk anal. (PRA) for risk-informed applications aimed to emphasize both
     effective risk control and effective resource expenditures at NPPs.
     TS&M-related parameters in a plant are assocd. with controlling risk or
     with satisfying requirements, and are candidates to be evaluated for their
     resource effectiveness in risk-informed applications.  The resource vs.
     risk-control effectiveness principles formally enter in optimization
     problems where the cost or the burden for the plant staff is to be
     minimized while the risk or the availability of the safety equipment is
     constrained to be at a given level, and vice versa.  Optimization of TS&M
     has been found to be interesting from the very beginning.  However, the
     resoln. of such a kind of optimization problem has been limited to focus
     on only individual TS&M-related parameters (STI, AOT, PM frequency, etc.)
     and/or adopting an individual optimization criterion (availability, costs,
     plant risks, etc.).  Nevertheless, a no. of reasons exist (e.g.,
     interaction, similar scope, etc.) that justify the growing interest in the
     last years to focus on the simultaneous and multi-criteria optimization of
     TS&M.  In the simultaneous optimization of TS&M-related parameters based
     on risk (or unavailability) and cost, like in many other engineering
     optimization problems, one normally faces multi-modal and non-linear
     objective functions and a variety of both linear and non-linear
     constraints.  Genetic algorithms (GAs) have proved their capability to
     solve these kinds of problems, although GAs are essentially unconstrained
     optimization techniques that require adaptation for the intended

constrained optimization, where TS&M-related parameters act as the
decision variables.  This paper encompasses the problem formulation where
the objective function is derived and constraints that apply in the
simultaneous and multi-criteria optimization of TS&M activities based on
risk and cost functions at system level.  Fundamentals of a steady-state
GA (**SSGA**) as an optimization method are given which satisfies
the above requirements, paying special attention to its use in constrained
optimization problems.  A simple case of application is provided, focusing
on TS&M-related parameters optimization for a stand-by safety-related
system, which demonstrates how the **SSGA**-based optimization
approach works at the system level, providing practical and complete
alternatives beyond only math. solns. to a particular parameter.

REFERENCE COUNT:            48     THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS
                                   RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT


L2    ANSWER 9 OF 20    SCISEARCH    COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER:      2001:299474   SCISEARCH
THE GENUINE ARTICLE:   416EA
TITLE:                 Designing communication networks topologies using
                       steady-state genetic algorithms
AUTHOR:                Sayoud H (Reprint); Takahashi K; Vaillant B
CORPORATE SOURCE:      Multimedia Univ, CHBN, Fac Engn, Cyberjaya 63100, Malaysia
                       (Reprint)
COUNTRY OF AUTHOR:     Malaysia
SOURCE:                IEEE COMMUNICATIONS LETTERS, (MAR 2001) Vol. 5, No. 3, pp.
                       113-115.
                       Publisher: IEEE-INST ELECTRICAL ELECTRONICS ENGINEERS INC,
                       345 E 47TH ST, NEW YORK, NY 10017-2394 USA.
                       ISSN: 1089-7798.
DOCUMENT TYPE:         Article; Journal
LANGUAGE:              English
REFERENCE COUNT:       4
                       *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB      This letter presents the application of steady state genetic algorithms
        (**SSGA**) to minimize the total installation cost of a
        communication network by optimally designing the topology layout and
        assigning the corresponding capacities (TDCA problem). This highly
        constrained optimization problem is shown to be better solved using GA's.
        A binary representation of links between node pairs is developed and
        tested on a network of 20 nodes. Improved results, both in terms of
        network cost, performance and computation speed, are obtained when
        comparing with existing heuristic approaches.

L2    ANSWER 10 OF 20    CAPLUS    COPYRIGHT 2003 ACS
ACCESSION NUMBER:       2000:15369   CAPLUS
DOCUMENT NUMBER:        132:77661
TITLE:                  Lessening branching and increasing fragmentation when
                        culturing filamentous microorganisms to improve ease
                        of handling
INVENTOR(S):            Van Wezel, Gilles Philippus; Kraal, Barend; Luiten,
                        Rudolf Gijsbertus Maria
PATENT ASSIGNEE(S):     Rijksuniversiteit te Leiden, Neth.; Nederlandse
                        Organisatie voor Wetenschappelijk Onderzoek/Chemische
                        Wetenschap
SOURCE:                 PCT Int. Appl., 59 pp.
                        CODEN: PIXXD2
DOCUMENT TYPE:          Patent
LANGUAGE:               English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------|------|------|-----------------|------|
| WO 2000000613 | A1 | 20000106 | WO 1999-NL395 | 19990625 |

AB   A method of altering the growth habit of filamentous microorganisms in
     liq. culture to limit branching and increase fragmentation with a
     consequent improvement in liq. culturing properties is described.  This is
     achieved by introducing the **ssgA** gene of Streptomyces griseus
     into the microorganism, in particular filamentous fungi.  The **ssgA**
     gene originally found in S. griseus is found in a limited no. of other
     Streptomycetes, all of which showed sporulation in submerged culture or at
     least parts of the process.  Expression of the gene in Streptomyces
     coelicolor changed the growth habit from large mycelial lumps to strongly
     limited branching, frequent septation, and fragmented growth.

REFERENCE COUNT:          2      THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS
                                 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB   A method (I) for reducing the branching and fragment septation and/or
     enhancing fragmentation in filamentous bacteria during growth in a liquid
     culture medium, which involves providing a bacterium that expresses
     heterologous **SsgA**-activity, which in Streptomyces griseus is
     encoded by an **ssgA** gene that is encoded by at least a 438 bp
     DNA sequence (specified), is new.  Also claimed are a filamentous
     bacterium (II) obtained using (I) and a method for producing an
     antibiotic or useful protein which involves culturing (II) (especially in
     a submerged culture) and the harvesting the antibiotic or protein from
     the culture.  (I) may be useful for altering the growth of filamentous
     bacteria in submerged cultures, which may be useful for improving the
     production of heterologous proteins and products by the bacterium.  These
     products include secondary metabolites such as antibiotics, antitumor
     agents, immunosuppressive agents, hypocholesterolemic agents,

enzyme-inhibitors, antimigraine agents, herbicides, useful proteins, etc.
In an example, vector plasmid pGWS2 and plasmid pGWS3, which contained
the **ssgA** gene, were used to transform Streptomyces coelicolor
M145 cells.  (60pp)

L2   ANSWER 12 OF 20   CAPLUS  COPYRIGHT 2003 ACS       DUPLICATE 4
ACCESSION NUMBER:         2000:722097  CAPLUS
DOCUMENT NUMBER:          134:2464
TITLE:                    **ssgA** is essential for sporulation of
                          Streptomyces coelicolor A3(2) and affects hyphal
                          development by stimulating septum formation
AUTHOR(S):                Van Wezel, Gilles P.; Van der Meulen, Jannes;
                          Kawamoto, Shinichi; Luiten, Ruud G. M.; Koerten, Henk
                          K.; Kraal, Barend
CORPORATE SOURCE:         Leiden Institute of Chemistry, Leiden University,
                          Leiden, 2300 RA, Neth.
SOURCE:                   Journal of Bacteriology (2000), 182(20), 5653-5662
                          CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER:                American Society for Microbiology
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
AB    The role of **ssgA** in cell division and development of
      streptomycetes was analyzed.  An **ssgA** null mutant of S.
      coelicolor produced aerial hyphae but failed to sporulate, and
      **ssgA** can therefore be regarded as a novel whi gene.  In addn. to
      the morphol. changes, antibiotic prodn. was also disturbed, with strongly
      reduced actinorhodin prodn.  These defects could be complemented by
      plasmid-borne **ssgA**.  In the wild-type strain, transcription of
      **ssgA** was induced by nutritional shift-down and was shown to be
      linked to that of the upstream-located gene ssgR, which belongs to the
      family of iclR-type transcriptional regulator genes.  Anal. of mycelium
      harvested from liq.-grown cultures by transmission electron microscopy
      showed that septum formation had strongly increased in **ssgA**
      -overexpressing strains in comparison to wild-type S. coelicolor and that
      spore-like compartments were produced at high frequency.  Furthermore, the
      hyphae were significantly wider and contained irregular and often
      extremely thick septa.  These data underline the important role for
      **ssgA** in Streptomyces cell division.
REFERENCE COUNT:          42    THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS
                                RECORD.  ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2   ANSWER 13 OF 20   CAPLUS  COPYRIGHT 2003 ACS       DUPLICATE 5
ACCESSION NUMBER:         2000:688832  CAPLUS
DOCUMENT NUMBER:          134:142568
TITLE:                    Characterization of ssfR and **ssgA**, two genes
                          involved in sporulation of Streptomyces griseus
AUTHOR(S):                Jiang, Hao; Kendrick, Kathleen E.
CORPORATE SOURCE:         Department of Microbiology, The Ohio State University,
                          Columbus, OH, 43210, USA
SOURCE:                   Journal of Bacteriology (2000), 182(19), 5521-5529
                          CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER:                American Society for Microbiology
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
AB    In the presence of cefoxitin, which inhibits septum formation during
      sporulation, Streptomyces griseus is unable to sporulate, retaining the
      sonication sensitivity of nonsporulating hyphae.  Cefoxitin- and
      sonication-resistant mutant SKK2600 was isolated and showed many morphol.
      differences from its parental strain.  A 3.6-kb DNA fragment that
      complemented the mutations of SKK2600 contained two open reading frames
      (ORFs), either of which could complement SKK2600.  One ORF, designated
      ssfR, encoded a protein contg. a potential DNA-binding helix-turn-helix
      motif close to its N terminus.  SsfR is similar to members of a large
      family of transcriptional regulators, particularly IcIR of Escherichia

coli. The second ORF was identified as **ssgA**, a previously
described sporulation gene from S. griseus. A point mutation of C to T
seven nucleotides upstream of the UGA stop codon of ssfR was responsible
for the phenotype of isolated mutant strain SKK2600. Surprisingly, this
mutation should not change the primary structure of SsfR. The ssfR and
**ssgA** disruption mutants were constructed and showed the "white"
mutant phenotype, with some growth medium dependence. In addn., the ssfR
null mutant sporulated ectopically in phosphate starvation medium.
REFERENCE COUNT:          36    THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS
                                RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT


L2    ANSWER 14 OF 20  BIOSIS   COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE
      6
ACCESSION NUMBER:      2001:21570  BIOSIS
DOCUMENT NUMBER:       PREV200100021570
TITLE:                 Continuous monitoring of single-sweat-gland activity.
AUTHOR(S):             Shamsuddin, A. K. M. (1); Togawa, Tatsuo
CORPORATE SOURCE:      (1) Nuclear Medicine Centre, Chittagong Medical College
                       Hospital Campus, Chittagong: akmshams@abnetbd.com
                       Bangladesh
SOURCE:                Physiological Measurement, (November, 2000) Vol. 21, No. 4,
                       pp. 535-540. print.
                       ISSN: 0967-3334.
DOCUMENT TYPE:         Article
LANGUAGE:              English
SUMMARY LANGUAGE:      English
AB    A conductivity measurement system using a small ion-free-solution
      perfusion chamber has been developed to monitor single-sweat-gland
      activity (**SSGA**) continuously at the skin surface. The chamber
      has a small open space of 0.2 mm2 at the bottom and has a transparent
      window. Single sweat pores were visualized by the starch/iodine method and
      the chamber was attached onto a single sweat pore using a magnifying lens
      affixed at the window. Silver electrodes were installed inside the
      chamber, and, by perfusing ion-free solution through the chamber at a
      constant flow rate, the conductivity of the solution was measured at the
      inlet and the outlet of the chamber. Continuous **SSGA** was
      monitored at the palm, finger tip and chest skin surface when the subjects
      were seated in a resting position and under stresses such as hand grasping
      with a dynamometer and performing mental arithmetic. Different types of
      response were observed from different sweat pores. The response time of
      this system was less than 0.15 s. The present results reveal that
      continuous sweat activity can be monitored even from a single sweat gland.


L2    ANSWER 15 OF 20  CAPLUS   COPYRIGHT 2003 ACS          DUPLICATE 7
ACCESSION NUMBER:      2001:407287  CAPLUS
DOCUMENT NUMBER:       135:132924
TITLE:                 Effects of increased and deregulated expression of
                       cell division genes on the morphology and on
                       antibiotic production of Streptomycetes
AUTHOR(S):             van Wezel, Gilles P.; van der Meulen, Jannes; Taal,
                       Elly; Koerten, Henk; Kraal, Barend
CORPORATE SOURCE:      Department of Biochemistry, Leiden Institute of
                       Chemistry, Leiden University, Leiden, 2300 RA, Neth.
SOURCE:                Antonie van Leeuwenhoek (2000), 78(3-4), 269-276
                       CODEN: ALJMAO; ISSN: 0003-6072
PUBLISHER:             Kluwer Academic Publishers
DOCUMENT TYPE:         Journal
LANGUAGE:              English
AB    This paper describes the effects of increased expression of the cell
      division genes ftsZ, ftsQ, and **ssgA** on the development of both
      solid- and liq.-grown mycelium of Streptomyces coelicolor and Streptomyces
      lividans. Over-expression of ftsZ in S. coelicolor M145 inhibited aerial
      mycelium formation and blocked sporulation. Such deficient sporulation
      was also obsd. for the ftsZ mutant. Over-expression of ftsZ also

inhibited morphol. differentiation in S. lividans 1326, although aerial
mycelium formation was less reduced. Furthermore, antibiotic prodn. was
increased in both strains, and in particular the otherwise dormant
actinorhodin biosynthesis cluster of S. lividans was activated in liq.-
and solid-grown cultures. No significant alterations were obsd. when the
gene dosage of ftsQ was increased. Anal. by transmission electron
microscopy of an S. coelicolor strain overexpressing **ssgA** showed
that septum formation had strongly increased in comparison to wild-type S.
coelicolor, showing that **SsgA** clearly influences Streptomyces
cell division. The morphol. of the hyphae was affected such that
irregular septa were produced with a significantly wider diam., thereby
forming spore-like compartments. This suggests that **ssgA** can
induce a process similar to submerged sporulation in Streptomyces strains
that otherwise fail to do so. A working model is proposed for the
regulation of septum formation and of submerged sporulation.
REFERENCE COUNT:          35     THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS
                                 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

ACCESSION NUMBER:       2000:175072   SCISEARCH
THE GENUINE ARTICLE:    287HW
TITLE:                  Constrained optimization of test intervals using a
                        steady-state genetic algorithm
AUTHOR:                 Martorell S (Reprint); Carlos S; Sanchez A; Serradell V
CORPORATE SOURCE:       UNIV POLITECN VALENCIA, DEPT INGN QUIM & NUCL, POB 22012,
                        E-46071 VALENCIA, SPAIN (Reprint)
COUNTRY OF AUTHOR:      SPAIN
SOURCE:                 RELIABILITY ENGINEERING & SYSTEM SAFETY, (MAR 2000) Vol.
                        67, No. 3, pp. 215-232.
                        Publisher: ELSEVIER SCI LTD, THE BOULEVARD, LANGFORD LANE,
                        KIDLINGTON, OXFORD OX5 1GB, OXON, ENGLAND.
                        ISSN: 0951-8320.
DOCUMENT TYPE:          Article; Journal
FILE SEGMENT:           ENGI
LANGUAGE:               English
REFERENCE COUNT:        42
                        *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
AB        There is a growing interest from both the regulatory authorities and
          the nuclear industry to stimulate the use of Probabilistic Risk Analysis
          (PRA) for risk-informed applications at Nuclear Power Plants (NPPs).
          Nowadays, special attention is being paid on analyzing plant-specific
          changes to Test Intervals (TIs) within the Technical Specifications (TSs)
          of NPPs and it seems to be a consensus on the need of making these
          requirements more risk-effective and less costly. Resource versus
          risk-control effectiveness principles formally enters in optimization
          problems. This paper presents an approach for using the PRA models in
          conducting the constrained optimization of TIs based on a steady-state
          genetic algorithm (**SSGA**) where the cost or the burden is to be
          minimized while the risk or performance is constrained to be at a given
          level, or vice versa. The paper encompasses first with the problem
          formulation, where the objective function and constraints that apply in
          the constrained optimization of TIs based on risk and cost models at
          system level are derived. Next, the foundation of the optimizer is given,
          which is derived by customizing a **SSGA** in order to allow
          optimizing TIs under constraints. Also, a case study is performed using
          this approach, which shows the benefits of adopting both PRA models and
          genetic algorithms, in particular for the constrained optimization of TIs,
          although it is also expected a great benefit of using this approach to
          solve other engineering optimization problems. However, care must be taken
          in using genetic algorithms in constrained optimization problems as it is
          concluded in this paper. (C) 2000 Elsevier Science Ltd. All rights
          reserved.

ACCESSION NUMBER:     1999:536541   SCISEARCH
THE GENUINE ARTICLE:  213EH
TITLE:                Identification of a three-amino acid deletion in the
                      alpha(2B)-adrenergic receptor that is associated with
                      reduced basal metabolic rate in obese subjects
AUTHOR:               Heinonen P; Koulu M (Reprint); Pesonen U; Karvonen M K;
                      Rissanen A; Laakso M; Valve R; Uusitupa M; Scheinin M
CORPORATE SOURCE:     UNIV TURKU, DEPT PHARMACOL & CLIN PHARMACOL,
                      KIINAMYLLYNKATU 10, FIN-20520 TURKU, FINLAND (Reprint);
                      UNIV TURKU, DEPT PHARMACOL & CLIN PHARMACOL, FIN-20520
                      TURKU, FINLAND; HELSINKI UNIV HOSP, EATING DISORDER UNIT,
                      FIN-00250 HELSINKI, FINLAND; UNIV KUOPIO, DEPT MED,
                      FIN-70211 KUOPIO, FINLAND; UNIV KUOPIO, DEPT CLIN NUTR,
                      FIN-70211 KUOPIO, FINLAND
COUNTRY OF AUTHOR:    FINLAND
SOURCE:               JOURNAL OF CLINICAL ENDOCRINOLOGY AND METABOLISM, (JUL
                      1999) Vol. 84, No. 7, pp. 2429-2433.
                      Publisher: ENDOCRINE SOC, 4350 EAST WEST HIGHWAY SUITE
                      500, BETHESDA, MD 20814-4110.
                      ISSN: 0021-972X.
DOCUMENT TYPE:        Article; Journal
FILE SEGMENT:         LIFE; CLIN
LANGUAGE:             English
REFERENCE COUNT:      29
                      *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB    The alpha(2)-adrenergic receptors mediate part of the actions of the
catecholamines noradrenaline and adrenaline on the regulation of energy
balance. As part of an ongoing study on the genetics of obesity, the
entire coding sequence of the alpha(2B)-adrenoceptor gene was screened in
58 obese, nondiabetic Finns by FOR-single stranded conformational analysis
(PGR-SSGA). A polymorphism that leads to a deletion of 3
glutamic acids from a glutamic acid repeat element (Glu x 12, amino acids
297-309) present in the third intracellular loop of the receptor protein
was identified. This repeat element has previously been shown to be
important for agonist-dependent receptor desensitization. Of 166 genotyped
subjects, 47 (28%) had 2 normal (long) alleles (Glu(12)/Glu(12)), 90 (54%)
were heterozygous (Glu(12)/Glu(9)), and 29 (17%) were homozygous for the
short (Glu(9)/Glu(9)) form. The basal metabolic rate, determined by
indirect calorimetry and adjusted for fat-free body mass, fat mass, sex,
and age, was 94 Cal/day (5.6%) lower (95% confidence interval for
difference, 32, 156) in subjects homozygous for the short allele than in
subjects with two long alleles (F = 4.84; P = 0.009, by ANOVA). Thus, a
genetic polymorphism of the alpha(2B)-adrenoceptor subtype can partly
explain the variation in basal metabolic rate in an obese population and
may therefore contribute to the pathogenesis of obesity.

L2   ANSWER 18 OF 20   CAPLUS   COPYRIGHT 2003 ACS        DUPLICATE 8
ACCESSION NUMBER:        1998:518346   CAPLUS
DOCUMENT NUMBER:         129:200360
TITLE:                   Complementation of the Mpg1 mutant phenotype in
                         Magnaporthe grisea reveals functional relationships
                         between fungal hydrophobins
AUTHOR(S):               Kershaw, Michael J.; Wakley, Gavin; Talbot, Nicholas
                         J.
CORPORATE SOURCE:        Department of Biological Sciences, Washington Singer
                         Laboratories, University of Exeter, Exeter, EX4 4QG,
                         UK
SOURCE:                  EMBO Journal (1998), 17(14), 3838-3849
                         CODEN: EMJODG; ISSN: 0261-4189
PUBLISHER:               Oxford University Press
DOCUMENT TYPE:           Journal
LANGUAGE:                English
AB    The functional relationship between fungal hydrophobins was studied by
      complementation anal. of an mpg1- gene disruption mutant in Magnaporthe

grisea.  MPG1 encodes a hydrophobin required for full pathogenicity of the
fungus, efficient elaboration of its infection structures and conidial
rodlet protein prodn.  Seven heterologous hydrophobin genes were selected
which play distinct roles in conidiogenesis, fruit body development,
aerial hyphae formation and infection structure elaboration in diverse
fungal species.  Each hydrophobin was introduced into an mpg1- mutant by
transformation.  Only one hydrophobin gene, SC1 from Schizophyllum
commune, was able partially to complement mpg1- mutant phenotypes when
regulated by its own promoter.  In contrast, six of the transformants
expressing hydrophobin genes controlled by the MPG1 promoter (SC1 and SC4
from S.commune, rodA and dewA from Aspergillus nidulans, EAS from
Neurospora crassa and **ssgA** from Metarhizium anisopliae) could
partially complement each of the diverse functions of MPG1.
Complementation was always assocd. with partial restoration of a rodlet
protein layer, characteristic of the particular hydrophobin being
expressed, and with hydrophobin surface assembly during infection
structure formation.  This provides the first genetic evidence that
diverse hydrophobin-encoding genes encode functionally related proteins
and suggests that, although very diverse in amino acid sequence, the
hydrophobins constitute a closely related group of morphogenetic proteins.
REFERENCE COUNT:           40     THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS
                                  RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT


L2    ANSWER 19 OF 20   CAPLUS   COPYRIGHT 2003 ACS          DUPLICATE 9
ACCESSION NUMBER:          1997:301915   CAPLUS
DOCUMENT NUMBER:           127:15298
TITLE:                     Expression analysis of the **ssgA** gene
                           product, associated with sporulation and cell division
                           in Streptomyces griseus
AUTHOR(S):                 Kawamoto, Shinichi; Watanabe, Hajime; Hesketh, Andrew;
                           Ensign, Jerald C.; Ochi, Kozo
CORPORATE SOURCE:          National Food Research Institute, Ibaraki, 305, Japan
SOURCE:                    Microbiology (Reading, United Kingdom) (1997), 143(4),
                           1077-1086
                           CODEN: MROBEO; ISSN: 1350-0872
PUBLISHER:                 Society for General Microbiology
DOCUMENT TYPE:             Journal
LANGUAGE:                  English
AB    The **ssgA** gene of Streptomyces griseus B2682, when present in
      high copy no., results in both suppression of sporulation and fragmented
      growth of mycelia.  Western anal. with polyclonal antibodies against the
      gene product (**SsgA**) revealed a close correlation between
      **SsgA** accumulation and the onset of sporulation in wild-type cells.
      The protein was only detected in the cytoplasm.  Certain developmental
      mutants of S. griseus (afs, relC and brgA) which are defective in aerial
      mycelium formation in solid culture and submerged spore formation in liq.
      culture failed to accumulate **SsgA**.  The **SsgA** protein
      appeared shortly (1 h) after nutritional shift-down of strain B2682 cells.
      Afs mutant cells sporulated and expressed **SsgA** only when
      A-factor was present both before and after nutritional shift-down.
      Introduction of the **ssgA** gene in a low-copy-no. vector into
      strain B2682 resulted in fivefold overexpression of **SsgA**, and
      was accompanied by fragmented growth of mycelia and suppression of
      submerged spore formation (in liq. culture) and aerial mycelium formation
      (in solid culture).  Streptomycin prodn. was not inhibited.  In a control
      expt., a nonfunctional **ssgA** gene possessing a frameshift
      mutation near its N-terminus had no effect on either growth or
      sporulation.  It is proposed that the **ssgA** gene product plays a
      role in promoting the developmental process of S. griseus.


L2    ANSWER 20 OF 20   CAPLUS   COPYRIGHT 2003 ACS          DUPLICATE 10
ACCESSION NUMBER:          1993:465878   CAPLUS
DOCUMENT NUMBER:           119:65878
TITLE:                     Cloning and regulatory analysis of starvation-stress

gene, **ssgA**, encoding a hydrophobin-like
protein from the entomopathogenic fungus, Metarhizium
anisopliae

AUTHOR(S):           St. Leger, Raymond J.; Staples, Richard C.; Roberts,
Donald W.

CORPORATE SOURCE:     Boyce Thompson Inst. Plant Res., Inc., Ithaca, NY,
14853-1801, USA

AB    The nucleotide (nt) sequence of a starvation-stress gene (**ssgA**)
of the entomopathogenic fungus, M. anisopliae, and its deduced amino acid
(aa) sequence were detd. The primary structure of the **SSGA** (96
aa; deduced Mr = 9925; pI = 4.1) protein shares extensive similarities
with fungal wall proteins of the hydrophobin class, and the eight Cys
residues and putative signal sequences are conserved. Secondary structure
predictions suggest an addnl. resemblance to low-Mr toxins and
agglutinins. Northern (RNA) blot anal. and nuclear run-on assays
demonstrated transcriptional control of expression of **ssgA**
during nutrient deprivation and during formation of infection structures.
Hybridizations of M. anisopliae genomic DNA indicate that there is only
one form of **ssgA** in the genome.

```
=> d his

        (FILE 'HOME' ENTERED AT 09:43:06 ON 22 JAN 2003)

        FILE 'CAPLUS, BIOSIS, EMBASE, MEDLINE, SCISEARCH, BIOTECHNO, BIOTECHDS'
        ENTERED AT 09:43:44 ON 22 JAN 2003
L1              62 S SSGA
L2              20 DUP REM L1 (42 DUPLICATES REMOVED)
```

Generate Collection | Print

TITLE: Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties

Basic Abstract Text (1):
NOVELTY - Novel method (I) for reducing branching and fragment septation and/or enhancing fragmentation in filamentous bacteria during growth in a liquid medium. Comprises providing a bacterium that has or expresses heterologous SsgA-activity, which in Streptomyces griseus is encoded by a ssgA gene that has at least a 438 bp sequence (fully defined in the specification).

Basic Abstract Text (6):
ADVANTAGE - (I) allows easy integration of the ssgA gene into the chromosome of the bacterium, resulting in high stability and independent regulation of ssgA. In this way, (I) reduces branching and fragment septation and enhances fragmentation of the mycelium in liquid culture, resulting in lower viscosity of culture broths and allowing high yields of useful products produced by the bacteria to be maintained.

Equivalent Abstract Text (1):
NOVELTY - Novel method (I) for reducing branching and fragment septation and/or enhancing fragmentation in filamentous bacteria during growth in a liquid medium. Comprises providing a bacterium that has or expresses heterologous SsgA-activity, which in Streptomyces griseus is encoded by a ssgA gene that has at least a 438 bp sequence (fully defined in the specification).

Equivalent Abstract Text (6):
ADVANTAGE - (I) allows easy integration of the ssgA gene into the chromosome of the bacterium, resulting in high stability and independent regulation of ssgA. In this way, (I) reduces branching and fragment septation and enhances fragmentation of the mycelium in liquid culture, resulting in lower viscosity of culture broths and allowing high yields of useful products produced by the bacteria to be maintained.

Generate Collection        Print

## Search Results - Record(s) 1 through 18 of 18 returned.

☐ 1.   Document ID: US 20020086412 A1

L1: Entry 1 of 18                               File: PGPB                          Jul 4, 2002

PGPUB-DOCUMENT-NUMBER: 20020086412
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020086412 A1

TITLE: Reducing branching and enhancing fragmentation in culturing filamentous
microorganisms

PUBLICATION-DATE: July 4, 2002

INVENTOR-INFORMATION:
| NAME | CITY | STATE | COUNTRY | RULE-47 |
|------|------|-------|---------|---------|
| van Wezel, Gilles Philippus | Leiden | | NL | |
| Kraal, Barend | Leiden | | NL | |
| Luiten, Rudolf Gijsbertus, M. | Leiden | | NL | |

US-CL-CURRENT: 435/252.1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

---

☐ 2.   Document ID: US 6272465 B1

L1: Entry 2 of 18                               File: USPT                          Aug 7, 2001

US-PAT-NO: 6272465
DOCUMENT-IDENTIFIER: US 6272465 B1

TITLE: Monolithic PC audio circuit

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

---

☐ 3.   Document ID: US 6246774 B1

L1: Entry 3 of 18                               File: USPT                          Jun 12, 2001

US-PAT-NO: 6246774
DOCUMENT-IDENTIFIER: US 6246774 B1

TITLE: Wavetable audio synthesizer with multiple volume components and two modes of stereo
positioning

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

---

☐ 4.   Document ID: US 6064743 A

L1: Entry 4 of 18                               File: USPT                          May 16, 2000

US-PAT-NO: 6064743
DOCUMENT-IDENTIFIER: US 6064743 A

TITLE: Wavetable audio synthesizer with waveform volume control for eliminating zipper noise

`Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image`

---

☐ 5. Document ID: US 6058066 A

L1: Entry 5 of 18                    File: USPT                    May 2, 2000

US-PAT-NO: 6058066
DOCUMENT-IDENTIFIER: US 6058066 A

TITLE: Enhanced register array accessible by both a system microprocessor and a wavetable audio synthesizer

`Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments      KWIC | Draw Desc | Image`

---

☐ 6. Document ID: US 6047073 A

L1: Entry 6 of 18                    File: USPT                    Apr 4, 2000

US-PAT-NO: 6047073
DOCUMENT-IDENTIFIER: US 6047073 A

TITLE: Digital wavetable audio synthesizer with delay-based effects processing

`Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments      KWIC | Draw Desc | Image`

---

☐ 7. Document ID: US 5864024 A

L1: Entry 7 of 18                    File: USPT                    Jan 26, 1999

US-PAT-NO: 5864024
DOCUMENT-IDENTIFIER: US 5864024 A

TITLE: Synthetic glycoamines and methods for their use that affect cell adhesion, inhibit cancer cell metastasis, and induce apoptosis

`Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments      KWIC | Draw Desc | Image`

---

☐ 8. Document ID: US 5809466 A

L1: Entry 8 of 18                    File: USPT                    Sep 15, 1998

US-PAT-NO: 5809466
DOCUMENT-IDENTIFIER: US 5809466 A

TITLE: Audio processing chip with external serial port

`Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments      KWIC | Draw Desc | Image`

---

☐ 9. Document ID: US 5742695 A

L1: Entry 9 of 18                    File: USPT                    Apr 21, 1998

US-PAT-NO: 5742695
DOCUMENT-IDENTIFIER: US 5742695 A

TITLE: Wavetable audio synthesizer with waveform volume control for eliminating zipper noise

`Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments`   `KWIC | Draw Desc | Image`

---

☐ 10.   Document ID: US 5717787 A

L1: Entry 10 of 18                    File: USPT                    Feb 10, 1998

US-PAT-NO: 5717787
DOCUMENT-IDENTIFIER: US 5717787 A

TITLE: Method for data compression by associating complex numbers with files of data values

`Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments`   `KWIC | Draw Desc | Image`

---

☐ 11.   Document ID: US 5675808 A

L1: Entry 11 of 18                    File: USPT                    Oct 7, 1997

US-PAT-NO: 5675808
DOCUMENT-IDENTIFIER: US 5675808 A

TITLE: Power control of circuit modules within an integrated circuit

`Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments`   `KWIC | Draw Desc | Image`

---

☐ 12.   Document ID: US 5668338 A

L1: Entry 12 of 18                    File: USPT                    Sep 16, 1997

US-PAT-NO: 5668338
DOCUMENT-IDENTIFIER: US 5668338 A

TITLE: Wavetable audio synthesizer with low frequency oscillators for tremolo and vibrato effects

`Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments`   `KWIC | Draw Desc | Image`

---

☐ 13.   Document ID: US 5659466 A

L1: Entry 13 of 18                    File: USPT                    Aug 19, 1997

US-PAT-NO: 5659466
DOCUMENT-IDENTIFIER: US 5659466 A

TITLE: Monolithic PC audio circuit with enhanced digital wavetable audio synthesizer

`Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments`   `KWIC | Draw Desc | Image`

---

☐ 14.   Document ID: US 5629412 A

US-PAT-NO: 5629412
DOCUMENT-IDENTIFIER: US 5629412 A

TITLE: Synthetic glycoamines that promote or inhibit cell adhesion

| Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments |     | KWIC | Draw Desc | Image |

---

☐   15.   Document ID:  US 4887049 A

L1: Entry 15 of 18                    File: USPT                    Dec 12, 1989

US-PAT-NO: 4887049
DOCUMENT-IDENTIFIER: US 4887049 A

TITLE: Solid state space harmonic amplifier

| Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments |     | KWIC | Draw Desc | Image |

---

☐   16.   Document ID:  JP 61258534 A

L1: Entry 16 of 18                    File: JPAB                    Nov 15, 1986

PUB-NO: JP361258534A
DOCUMENT-IDENTIFIER: JP 61258534 A
TITLE: DIGITAL SIGNAL DEMODULATOR

| Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments |     | KWIC | Draw Desc | Image |

---

☐   17.   Document ID:  EP 974657 A1

L1: Entry 17 of 18                    File: EPAB                    Jan 26, 2000

PUB-NO: EP000974657A1
DOCUMENT-IDENTIFIER: EP 974657 A1
TITLE: Reducing branching and enhancing fragmentation in culturing filamentous
microorganisms

| Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments |     | KWIC | Draw Desc | Image |

---

☐   18.   Document ID:  WO 200000613 A1 US 20020086412 A1 EP 974657 A1 AU 9946590 A EP
1090121 A1

L1: Entry 18 of 18                    File: DWPI                    Jan 6, 2000

DERWENT-ACC-NO: 2000-147269
DERWENT-WEEK: 200247
COPYRIGHT 2003 DERWENT INFORMATION LTD

TITLE: Reducing branching and enhancing fragmentation in filamentous microorganisms used to
improve their liquid culturing properties

| Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments |     | KWIC | Draw Desc | Image |

---

Generate Collection        Print

| Terms | Documents |
|-------|-----------|
| ssgA  | 18 |

**Display Format:** [ - ] [ Change Format ]

Previous Page      Next Page